

# SEQUENCE LISTING

<110> Christensen, Bjorn Eggert  
Mollgaard, Henrik  
Kaasgaard, Svend  
Lehmbeck, Jan

<120> Methods for producing polypeptides in  
aspergillus mutant cells

<130> 4483.200-US

<140> 09/472,364

<141> 1999-12-23

<150> 60/139,593

<151> 1999-06-17

<150> 60/117,396

<151> 1999-01-27

<150> PA 1999 00745

<151> 1999-05-27

<150> PA 1998 01726

<151> 1998-12-23

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1393

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 5956

<221> CDS

<222> (15)...(1328)

<400> 1

ccgaaagctg agca atg gag atc tcc aag aaa gca gca aca ctg ctg cca	50
Met Glu Ile Ser Lys Lys Ala Ala Thr Leu Leu Pro	
1 5 10	

aag ccc ttc tac gtg ctg agt caa gcc ctg aac ctc tcg aac aag gac	98
Lys Pro Phe Tyr Val Leu Ser Gln Ala Leu Asn Leu Ser Asn Lys Asp	
15 20 25	

cac aca aaa tgg tgg tat agc aca gct ccg atg ttt gcc acc atg atg	146
His Thr Lys Trp Trp Tyr Ser Thr Ala Pro Met Phe Ala Thr Met Met	
30 35 40	

gcg ggg gcc ggc tat gat gtt cac gca cag tac aag ttc ctc tgt atc	194
Ala Gly Ala Gly Tyr Asp Val His Ala Gln Tyr Lys Phe Leu Cys Ile	
45 50 55 60	
cac cgt gag gtc atc atc ccg gcg ttg ggt cca tac cca gaa aag ggt	242
His Arg Glu Val Ile Ile Pro Ala Leu Gly Pro Tyr Pro Glu Lys Gly	
65 70 75	
cag ccc atg cac tgg aag agt cat ctc aca cgc ttc gga ctt cct ttc	290
Gln Pro Met His Trp Lys Ser His Leu Thr Arg Phe Gly Leu Pro Phe	
80 85 90	
gag ctg agc ttc aat tac tcc aaa tca cta cta cgg ttt gca ttc gag	338
Glu Leu Ser Phe Asn Tyr Ser Lys Ser Leu Leu Arg Phe Ala Phe Glu	
95 100 105	
ccc ctc ggt tcc ctg acg gga acg aag gat gat cca ttc aac acc cag	386
Pro Leu Gly Ser Leu Thr Gly Thr Lys Asp Asp Pro Phe Asn Thr Gln	
110 115 120	
gca atc agg cct gtt ctc cag gac ctc aag gcc atg gtt cca ggg ctt	434
Ala Ile Arg Pro Val Leu Gln Asp Leu Lys Ala Met Val Pro Gly Leu	
125 130 135 140	
gac ctg gaa tgg ttc gat cat ttc act aaa gca ttg gtc gtt tcg gag	482
Asp Leu Glu Trp Phe Asp His Phe Thr Lys Ala Leu Val Val Ser Glu	
145 150 155	
gaa gag gct cgg act ctg cta gat cga gat att gag atc ccc gtc ttc	530
Glu Glu Ala Arg Thr Leu Leu Asp Arg Asp Ile Glu Ile Pro Val Phe	
160 165 170	
aag aca cag aac aaa ctg gca gcc gat ctg gag cca tct ggc gat att	578
Lys Thr Gln Asn Lys Leu Ala Ala Asp Leu Glu Pro Ser Gly Asp Ile	
175 180 185	
gtc ttg aag acc tac atc tac ccg cgg atc aag tcg atc gcg acc ggg	626
Val Leu Lys Thr Tyr Ile Tyr Pro Arg Ile Lys Ser Ile Ala Thr Gly	
190 195 200	
acc cca aaa gag aga ctc atg ttt gac gca atc aag gct gcc gac aag	674
Thr Pro Lys Glu Arg Leu Met Phe Asp Ala Ile Lys Ala Ala Asp Lys	
205 210 215 220	
ttt ggc aaa gtt gcc act cca ctg gca atc ctc gag gag ttt ata gct	722
Phe Gly Lys Val Ala Thr Pro Leu Ala Ile Leu Glu Glu Phe Ile Ala	
225 230 235	
gag cga gca ccc acc ctc ctc ggc cac ttt ctc tca tgc gat ttg gtc	770
Glu Arg Ala Pro Thr Leu Leu Gly His Phe Leu Ser Cys Asp Leu Val	
240 245 250	
aag ccg tcc gag tcc cga atc aag gtc tac tgt atg gaa cgc cag ctc	818
Lys Pro Ser Glu Ser Arg Ile Lys Val Tyr Cys Met Glu Arg Gln Leu	
255 260 265	
gac ctg gcc tcc atc gaa ggt att tgg act ctc aac ggg cga cgg aac	866

Asp	Leu	Ala	Ser	Ile	Glu	Gly	Ile	Trp	Thr	Leu	Asn	Gly	Arg	Arg	Asn		
270						275					280						
gat	cca	gag	aca	ctg	gat	ggg	ctg	gat	gcg	ctg	agg	gag	ctg	tgg	cag		914
Asp	Pro	Glu	Thr	Leu	Asp	Gly	Leu	Asp	Ala	Leu	Arg	Glu	Leu	Trp	Gln		
285					290				295						300		
cta	ttg	ccc	gtc	acg	gag	ggg	ctg	tgt	cca	ctg	ccg	aac	tgc	ttt	tac		962
Leu	Leu	Pro	Val	Thr	Glu	Gly	Leu	Cys	Pro	Leu	Pro	Asn	Cys	Phe	Tyr		
				305					310					315			
gag	ccg	ggg	acc	tca	ccg	cag	gag	cag	ctc	ccc	ttc	att	ata	aat	ttt		1010
Glu	Pro	Gly	Thr	Ser	Pro	Gln	Glu	Gln	Leu	Pro	Phe	Ile	Ile	Asn	Phe		
			320					325					330				
acc	ttg	tct	cct	aaa	agc	gca	ctt	ccc	gaa	cca	cag	atc	tat	ttc	cct		1058
Thr	Leu	Ser	Pro	Lys	Ser	Ala	Leu	Pro	Glu	Pro	Gln	Ile	Tyr	Phe	Pro		
			335				340					345					
gct	ttt	ggg	cag	aac	gac	aaa	acc	atc	gcg	gaa	gga	ttg	gcc	acc	ttc		1106
Ala	Phe	Gly	Gln	Asn	Asp	Lys	Thr	Ile	Ala	Glu	Gly	Leu	Ala	Thr	Phe		
			350			355					360						
ttt	gag	agc	aga	ggg	tgg	ggg	ggc	ttg	gct	aag	agc	tat	cca	gcg	gat		1154
Phe	Glu	Ser	Arg	Gly	Trp	Gly	Gly	Leu	Ala	Lys	Ser	Tyr	Pro	Ala	Asp		
365					370					375					380		
ttg	gca	tcc	tac	tat	ccc	gat	gtg	gac	ctg	cag	acc	gca	aat	cac	ctg		1202
Leu	Ala	Ser	Tyr	Tyr	Pro	Asp	Val	Asp	Leu	Gln	Thr	Ala	Asn	His	Leu		
				385					390					395			
cag	gcg	tgg	atc	tcc	ttc	tct	tac	aag	ggg	aaa	aaa	ccg	tac	atg	agt		1250
Gln	Ala	Trp	Ile	Ser	Phe	Ser	Tyr	Lys	Gly	Lys	Lys	Pro	Tyr	Met	Ser		
			400					405					410				
gtg	tac	ctc	cat	acc	ttc	gaa	gcg	ttc	agt	gct	gct	gcc	cag	gag	gtg		1298
Val	Tyr	Leu	His	Thr	Phe	Glu	Ala	Phe	Ser	Ala	Ala	Ala	Gln	Glu	Val		
			415				420					425					
gct	atg	tgt	cac	gat	ggc	cac	aat	cct	tag	gactagtttta tcccttcatt							1348
Ala	Met	Cys	His	Asp	Gly	His	Asn	Pro	*								
			430			435											
ctatgcatcc gttgaatgtg ttgggtcgaaa aaaaaaaaaa aaaaa																	1393

<210> 2  
 <211> 437  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Primer 5956

<400> 2  
 Met Glu Ile Ser Lys Lys Ala Ala Thr Leu Leu Pro Lys Pro Phe Tyr  
 1 5 10 15  
 Val Leu Ser Gln Ala Leu Asn Leu Ser Asn Lys Asp His Thr Lys Trp

			20					25					30			
Trp	Tyr	Ser	Thr	Ala	Pro	Met	Phe	Ala	Thr	Met	Met	Ala	Gly	Ala	Gly	
		35					40					45				
Tyr	Asp	Val	His	Ala	Gln	Tyr	Lys	Phe	Leu	Cys	Ile	His	Arg	Glu	Val	
	50				55					60						
Ile	Ile	Pro	Ala	Leu	Gly	Pro	Tyr	Pro	Glu	Lys	Gly	Gln	Pro	Met	His	
65					70					75					80	
Trp	Lys	Ser	His	Leu	Thr	Arg	Phe	Gly	Leu	Pro	Phe	Glu	Leu	Ser	Phe	
				85					90					95		
Asn	Tyr	Ser	Lys	Ser	Leu	Leu	Arg	Phe	Ala	Phe	Glu	Pro	Leu	Gly	Ser	
			100					105					110			
Leu	Thr	Gly	Thr	Lys	Asp	Asp	Pro	Phe	Asn	Thr	Gln	Ala	Ile	Arg	Pro	
		115					120					125				
Val	Leu	Gln	Asp	Leu	Lys	Ala	Met	Val	Pro	Gly	Leu	Asp	Leu	Glu	Trp	
	130					135					140					
Phe	Asp	His	Phe	Thr	Lys	Ala	Leu	Val	Val	Ser	Glu	Glu	Glu	Ala	Arg	
145					150					155					160	
Thr	Leu	Leu	Asp	Arg	Asp	Ile	Glu	Ile	Pro	Val	Phe	Lys	Thr	Gln	Asn	
				165					170					175		
Lys	Leu	Ala	Ala	Asp	Leu	Glu	Pro	Ser	Gly	Asp	Ile	Val	Leu	Lys	Thr	
			180					185					190			
Tyr	Ile	Tyr	Pro	Arg	Ile	Lys	Ser	Ile	Ala	Thr	Gly	Thr	Pro	Lys	Glu	
		195					200					205				
Arg	Leu	Met	Phe	Asp	Ala	Ile	Lys	Ala	Ala	Asp	Lys	Phe	Gly	Lys	Val	
	210					215					220					
Ala	Thr	Pro	Leu	Ala	Ile	Leu	Glu	Glu	Phe	Ile	Ala	Glu	Arg	Ala	Pro	
225					230					235					240	
Thr	Leu	Leu	Gly	His	Phe	Leu	Ser	Cys	Asp	Leu	Val	Lys	Pro	Ser	Glu	
				245					250					255		
Ser	Arg	Ile	Lys	Val	Tyr	Cys	Met	Glu	Arg	Gln	Leu	Asp	Leu	Ala	Ser	
			260					265					270			
Ile	Glu	Gly	Ile	Trp	Thr	Leu	Asn	Gly	Arg	Arg	Asn	Asp	Pro	Glu	Thr	
		275					280					285				
Leu	Asp	Gly	Leu	Asp	Ala	Leu	Arg	Glu	Leu	Trp	Gln	Leu	Leu	Pro	Val	
	290					295					300					
Thr	Glu	Gly	Leu	Cys	Pro	Leu	Pro	Asn	Cys	Phe	Tyr	Glu	Pro	Gly	Thr	
305					310					315					320	
Ser	Pro	Gln	Glu	Gln	Leu	Pro	Phe	Ile	Ile	Asn	Phe	Thr	Leu	Ser	Pro	
				325					330					335		
Lys	Ser	Ala	Leu	Pro	Glu	Pro	Gln	Ile	Tyr	Phe	Pro	Ala	Phe	Gly	Gln	
			340					345					350			
Asn	Asp	Lys	Thr	Ile	Ala	Glu	Gly	Leu	Ala	Thr	Phe	Phe	Glu	Ser	Arg	
		355					360					365				
Gly	Trp	Gly	Gly	Leu	Ala	Lys	Ser	Tyr	Pro	Ala	Asp	Leu	Ala	Ser	Tyr	
	370					375										

4

<213> Artificial Sequence

<220>

<223> Primer 5956

<400> 3

ggatccaggg ctccctggag

20

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 5955

<400> 4

cctgaccagc cagatctcct

20

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 6120

<400> 5

agtgagagaa ctccctcctc

20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 6121

<400> 6

ccatatcttc tcagttctcca

20